



ENTERED

PCT09

RAW SEQUENCE LISTING

DATE: 04/09/2002

PATENT APPLICATION: US/09/582,397A

TIME: 12:30:07

Input Set : A:\49862seq.txt

Output Set : N:\CRF3\04092002\I582397A.raw

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4 <110> APPLICANT: Shizuo AKIRA
5      Takahiro SHIMADA
7 <120> TITLE OF INVENTION: IDENTIFICATION OF NOVEL SUBSTRATE I-TRAF
8      OF IKK-i KINASE
10 <130> FILE REFERENCE: 49862 (71526)
12 <140> CURRENT APPLICATION NUMBER: 09/582,397A
13 <141> CURRENT FILING DATE: 2000-06-24
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17 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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20 <211> LENGTH: 2154
21 <212> TYPE: DNA
22 <213> ORGANISM: Human
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27 tcaacactac cagctacctg cgcccccgcg aggtgcaggt gagggagttt gaggtcctgc      180
28 ggaagctgaa ccaccagaac atcgtcaagc tctttgcggt ggaggagacg ggcggaagcc      240
29 ggcagaaggt actggtgatg gagtactgct ccagtgggag cctgctgagt gtgctggaga      300
30 gccctgagaa tgcctttggg ctgcctgagg atgagttcct ggtggtgctg cgctgtgtgg      360
31 tggccggcat gaaccacctg cgggagaacg gcattgtgca tcgcgacatc aagccgggga      420
32 acatcatgcg cctcgtaggg gaggaggggc agagcatcta caagctgaca gacttcggcg      480
33 ctgcccggga gctggatgat gatgagaagt tcgtctcggt ctatgggact gaggagtacc      540
34 tgcattccga catgtatgag cgggcgggtg ttcgaaagcc ccagcaaaaa gcgttcgggg      600
35 tgactgtgga tctctggagc attggagtga ccttgtacca tgcagccact ggcagcctgc      660
36 ccttcacccc ctttggtggg ccacggcgga acaaggagat catgtaccgg atcaccacag      720
37 agaagccggc tggggccatt gcaggtgccc agaggcgga gaacgggcc ctggagtgga      780
38 gctacaccct ccccatcacc tgccagctgt cactggggct gcagagccag ctggtgcca      840
39 tcctggccaa catcctggag gtggagcagg ccaagtgtg gggcttcgac cagttccttg      900
40 cggagaccag tgacatcctg cagcgagttg tcgtccatgt cttctccctg tcccaggcag      960
41 tcctgcacca catctatatc catgcccaca acacgatagc cattttccag gaggccgtgc      1020
42 acaagcagac cagtgtggcc ccccgacacc aggagtacct ctttgagggt cacctctgtg      1080
43 tcctcgagcc cagcgtctca gcacagcaca tcgcccacac gacggcaagc agccccctga      1140
44 ccctcttcag cacagccatc cctaaggggc tggccttcag ggaccctgct ctggacgtcc      1200
45 ccaagtctgt ccccaaagtg gacctgcagg cggattacaa cactgccaag ggcgtgttgg      1260
46 ggcgggcta ccaggccctg cggtggcac gggccctgct ggatgggcag gagctaattg      1320
47 ttcgggggct gactgggtc atggaggtgc tccaggccac atgcagacgg actctggaag      1380
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52 tccagcagat tcagtgtgtt ttggacaaga tgaacttcat ctacaaacag ttcaagaagt      1680
53 ctaggatgag gccagggtct ggctacaacg aggagcagat tcacaagctg gataaggtga      1740

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54 atttcagtca tttagccaaa agactcctgc aggtgttcca ggaggagtgc gtgcagaagt 1800
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56 acctgcgcct ggttggtgtg tctgtggctg cctgtaacac agaagcccag ggggtccagg 1920
57 agagtctcag caagctcctg gaagagctat ctcaccagct ccttcaggac cgagcaaagg 1980
58 gggctcaggc ctgcgcgcct cccatagctc cttacccag ccctacacga aaggacctgc 2040
59 ttctccacat gcaagagctc tgcgagggga tgaagctgct ggcattctgac ctctggaca 2100
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63 <211> LENGTH: 716
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65 <213> ORGANISM: Human
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71 20 25 30
72 Glu Leu Val Ala Val Lys Val Phe Asn Thr Thr Ser Tyr Leu Arg Pro
73 35 40 45
74 Arg Glu Val Gln Val Arg Glu Phe Glu Val Leu Arg Lys Leu Asn His
75 50 55 60
76 Gln Asn Ile Val Lys Leu Phe Ala Val Glu Glu Thr Gly Gly Ser Arg
77 65 70 75 80
78 Gln Lys Val Leu Val Met Glu Tyr Cys Ser Ser Gly Ser Leu Leu Ser
79 85 90 95
80 Val Leu Glu Ser Pro Glu Asn Ala Phe Gly Leu Pro Glu Asp Glu Phe
81 100 105 110
82 Leu Val Val Leu Arg Cys Val Val Ala Gly Met Asn His Leu Arg Glu
83 115 120 125
84 Asn Gly Ile Val His Arg Asp Ile Lys Pro Gly Asn Ile Met Arg Leu
85 130 135 140
86 Val Gly Glu Glu Gly Gln Ser Ile Tyr Lys Leu Thr Asp Phe Gly Ala
87 145 150 155 160
88 Ala Arg Glu Leu Asp Asp Glu Lys Phe Val Ser Val Tyr Gly Thr
89 165 170 175
90 Glu Glu Tyr Leu His Pro Asp Met Tyr Glu Arg Ala Val Leu Arg Lys
91 180 185 190
92 Pro Gln Gln Lys Ala Phe Gly Val Thr Val Asp Leu Trp Ser Ile Gly
93 195 200 205
94 Val Thr Leu Tyr His Ala Ala Thr Gly Ser Leu Pro Phe Ile Pro Phe
95 210 215 220
96 Gly Gly Pro Arg Arg Asn Lys Glu Ile Met Tyr Arg Ile Thr Thr Glu
97 225 230 235 240
98 Lys Pro Ala Gly Ala Ile Ala Gly Ala Gln Arg Arg Glu Asn Gly Pro
99 245 250 255
100 Leu Glu Trp Ser Tyr Thr Leu Pro Ile Thr Cys Gln Leu Ser Leu Gly
101 260 265 270
102 Leu Gln Ser Gln Leu Val Pro Ile Leu Ala Asn Ile Leu Glu Val Glu
103 275 280 285
104 Gln Ala Lys Cys Trp Gly Phe Asp Gln Phe Phe Ala Glu Thr Ser Asp

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106 Ile Leu Gln Arg Val Val His Val Phe Ser Leu Ser Gln Ala Val
107 305      310      315      320
108 Leu His His Ile Tyr Ile His Ala His Asn Thr Ile Ala Ile Phe Gln
109      325      330      335
110 Glu Ala Val His Lys Gln Thr Ser Val Ala Pro Arg His Gln Glu Tyr
111      340      345      350
112 Leu Phe Glu Gly His Leu Cys Val Leu Glu Pro Ser Val Ser Ala Gln
113      355      360      365
114 His Ile Ala His Thr Thr Ala Ser Ser Pro Leu Thr Leu Phe Ser Thr
115      370      375      380
116 Ala Ile Pro Lys Gly Leu Ala Phe Arg Asp Pro Ala Leu Asp Val Pro
117 385      390      395      400
118 Lys Phe Val Pro Lys Val Asp Leu Gln Ala Asp Tyr Asn Thr Ala Lys
119      405      410      415
120 Gly Val Leu Gly Ala Gly Tyr Gln Ala Leu Arg Leu Ala Arg Ala Leu
121      420      425      430
122 Leu Asp Gly Gln Glu Leu Met Phe Arg Gly Leu His Trp Val Met Glu
123      435      440      445
124 Val Leu Gln Ala Thr Cys Arg Arg Thr Leu Glu Val Ala Arg Thr Ser
125      450      455      460
126 Leu Leu Tyr Leu Ser Ser Ser Leu Gly Thr Glu Arg Phe Ser Ser Val
127 465      470      475      480
128 Ala Gly Thr Pro Glu Ile Gln Glu Leu Lys Ala Ala Ala Glu Leu Arg
129      485      490      495
130 Ser Arg Leu Arg Thr Leu Ala Glu Val Leu Ser Arg Cys Ser Gln Asn
131      500      505      510
132 Ile Thr Glu Thr Gln Glu Ser Leu Ser Ser Leu Asn Arg Glu Leu Val
133      515      520      525
134 Lys Ser Arg Asp Gln Val His Glu Asp Arg Ser Ile Gln Gln Ile Gln
135      530      535      540
136 Cys Cys Leu Asp Lys Met Asn Phe Ile Tyr Lys Gln Phe Lys Lys Ser
137 545      550      555      560
138 Arg Met Arg Pro Gly Leu Gly Tyr Asn Glu Glu Gln Ile His Lys Leu
139      565      570      575
140 Asp Lys Val Asn Phe Ser His Leu Ala Lys Arg Leu Leu Gln Val Phe
141      580      585      590
142 Gln Glu Glu Cys Val Gln Lys Tyr Gln Ala Ser Leu Val Thr His Gly
143      595      600      605
144 Lys Arg Met Arg Val Val His Glu Thr Arg Asn His Leu Arg Leu Val
145      610      615      620
146 Gly Cys Ser Val Ala Ala Cys Asn Thr Glu Ala Gln Gly Val Gln Glu
147 625      630      635      640
148 Ser Leu Ser Lys Leu Leu Glu Glu Leu Ser His Gln Leu Leu Gln Asp
149      645      650      655
150 Arg Ala Lys Gly Ala Gln Ala Ser Pro Pro Pro Ile Ala Pro Tyr Pro
151      660      665      670
152 Ser Pro Thr Arg Lys Asp Leu Leu His Met Gln Glu Leu Cys Glu
153      675      680      685

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154 Gly Met Lys Leu Leu Ala Ser Asp Leu Leu Asp Asn Asn Arg Ile Ile
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157 705                      710                      715
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160 <211> LENGTH: 2910
161 <212> TYPE: DNA
162 <213> ORGANISM: Mouse
164 <400> SEQUENCE: 3
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167 gaaatccggg gaggtggttg ctgtaaagggt cttcaactca gccagctatc ggcgacctcc      180
168 tgaggttcag gtgaggagggt ttgaggctct gcggaggctg aatcaccaga acatcgtgaa      240
169 gctattcgca gtggaggaaa cgggaggcag ccggcagaag gtgctaataca tggagtactg      300
170 ctccagtggg agcctgctga gcgtgctgga agaccctgag aacacgttcg ggctttctga      360
171 agaggagttc ctagtgggtgc tgcgctgtgt ggtggctggc atgaaccacc tgcgggagaa      420
172 tggcattgtc catcgggaca tcaaacctgg gaacatcatg cgctgggtgg gcgaggaggg      480
173 gcagagcatc tataagctgt ctgacttcgg ggcctgccgc aagctggacg atgatgagaa      540
174 gtttgtttct gtctatggta cagaggaata cctgcaccct gacatgtatg agcgtgcagt      600
175 gctgcgcaaa cccagcaaaa aggcatttgg tgtgactgtg gatctctgga gtattggggg      660
176 gacctgttac cacgcagcca caggcagctc gcccttcac ccttcggtg ggccccggcg      720
177 caacaaagag atcatgtaca gaatcaccac agagaagcca gccggggcca ttccagggac      780
178 tcagaagcag gaaaatggtc ccttgagggt gagctacagc ctccccatca cctgtagact      840
179 gtccatgggg ctgcagaacc agctgggtgc catcctggcc aacatcctgg aggtggaaga      900
180 ggataagtgc tggggctttg atcagttctt cgcggagacc agtgacattc tgcagcgaac      960
181 ggtcatccac gtcttttccc taccacaggg cgttttgcac catgtctaca tccacgcccc      1020
182 caacacgatt gccatctttt tggaggctgt atatgagcag accaacgtga ccccaaaaca      1080
183 ccaggagtac ctcttcgagg gtcacccttg tgtccttgag ccaagcctct cagcccagca      1140
184 catcgcccac acagctgcca gcagccctct aactctgttc agcatgtcca gcgacacacc      1200
185 taaggggctg gccttcaggg accctgctct ggatgtccca aagttcgtcc ctaaggttga      1260
186 cctacaggcc gattacagca cagctaaggg ggtgctgggc gctggctacc aggcctgtg      1320
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198 tgatcagctc cttctggaca gagcttccga acagggagct gaggtgtcac cgcaacctat      2040
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202 aatagaaaca ttcattattgt acccctacac tgtgagacca aattcagggc aagttctggt      2280
203 tccatctcac tagcctacct cctcttggc cattggccat tggccaacaa actagcatta      2340
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205 ctacagaaga gaccatgctg ctaccacagc cttatcaaga caccaagact gttcttcctt 2460
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207 tttccaggac cagcagcat ctctgtgctc ttctctgcc tctccagggt gctggatcag 2580
208 aatgcttatt cttcgttggt tctgtgctg ttctctgagt gtcccatcc cctggcctca 2640
209 ggcaaccac aaacggcccc tctgtgctg gtctagatgc acctgcattt gagaaagtgg 2700
210 gtggttgagg ctaactgctg gtgctttgag gattctcctt gaccttttct ccgaggaacg 2760
211 cttggttcta agaaacagct ggtcagtatc aaccacagcc atgctaactg gacagatgtt 2820
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215 <210> SEQ ID NO: 4
216 <211> LENGTH: 717
217 <212> TYPE: PRT
218 <213> ORGANISM: Mouse
220 <400> SEQUENCE: 4
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224 20 25 30
225 Glu Val Val Ala Val Lys Val Phe Asn Ser Ala Ser Tyr Arg Arg Pro
226 35 40 45
227 Pro Glu Val Gln Val Arg Glu Phe Glu Val Leu Arg Arg Leu Asn His
228 50 55 60
229 Gln Asn Ile Val Lys Leu Phe Ala Val Glu Glu Thr Gly Gly Ser Arg
230 65 70 75 80
231 Gln Lys Val Leu Ile Met Glu Tyr Cys Ser Ser Gly Ser Leu Leu Ser
232 85 90 95
233 Val Leu Glu Asp Pro Glu Asn Thr Phe Gly Leu Ser Glu Glu Glu Phe
234 100 105 110
235 Leu Val Val Leu Arg Cys Val Val Ala Gly Met Asn His Leu Arg Glu
236 115 120 125
237 Asn Gly Ile Val His Arg Asp Ile Lys Pro Gly Asn Ile Met Arg Leu
238 130 135 140
239 Val Gly Glu Glu Gly Gln Ser Ile Tyr Lys Leu Ser Asp Phe Gly Ala
240 145 150 155 160
241 Ala Arg Lys Leu Asp Asp Glu Lys Phe Val Ser Val Tyr Gly Thr
242 165 170 175
243 Glu Glu Tyr Leu His Pro Asp Met Tyr Glu Arg Ala Val Leu Arg Lys
244 180 185 190
245 Pro Gln Gln Lys Ala Phe Gly Val Thr Val Asp Leu Trp Ser Ile Gly
246 195 200 205
247 Val Thr Leu Tyr His Ala Ala Thr Gly Ser Leu Pro Phe Ile Pro Phe
248 210 215 220
249 Gly Gly Pro Arg Arg Asn Lys Glu Ile Met Tyr Arg Ile Thr Thr Glu
250 225 230 235 240
251 Lys Pro Ala Gly Ala Ile Ser Gly Thr Gln Lys Gln Glu Asn Gly Pro
252 245 250 255
253 Leu Glu Trp Ser Tyr Ser Leu Pro Ile Thr Cys Arg Leu Ser Met Gly
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VERIFICATION SUMMARY

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